

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/581,528 F
Source: EFW 16
Date Processed by STIC: 09/27/2005

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 09/27/2005

PATENT APPLICATION: US/09/581,528F

TIME: 15:21:56

Input Set : A:\P19743.txt

Output Set: N:\CRF4\09272005\I581528F.raw

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3 <110> APPLICANT: TAKEDA, Masatoshi
4     TAKEDA, Junji
6 <120> TITLE OF INVENTION: Gene-Mutated Animal
8 <130> FILE REFERENCE: P19743
10 <140> CURRENT APPLICATION NUMBER: 09/581,528F
11 <141> CURRENT FILING DATE: 2000-10-26
13 <150> PRIOR APPLICATION NUMBER: PCT/JP99/00015
14 <151> PRIOR FILING DATE: 1999-01-07
16 <150> PRIOR APPLICATION NUMBER: JP H10/2191
17 <151> PRIOR FILING DATE: 1998-01-08
19 <160> NUMBER OF SEQ ID NOS: 22
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 467
25 <212> TYPE: PRT
26 <213> ORGANISM: Human
28 <400> SEQUENCE: 1
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34 Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn
35          20          25          30
38 Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu
39          35          40          45
42 Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
43          50          55          60
46 Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
47 65          70          75          80
50 His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
51          85          90          95
54 Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
55          100         105         110
58 Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
59          115         120         125
62 Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
63          130         135         140
66 Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
67 145         150         155         160
70 Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
71          165         170         175
74 Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
75          180         185         190
78 Val Asp Tyr Ile Thr Val Ala Leu Ile Trp Asn Phe Gly Val Val
79          195         200         205

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82 Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
83      210                      215                      220
86 Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
87 225                      230                      235                      240
90 Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
91      245                      250                      255
94 Asp Leu Asp Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
95      260                      265                      270
98 Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
99      275                      280                      285
102 Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
103      290                      295                      300
106 Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr
107 305                      310                      315                      320
110 Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
111      325                      330                      335
114 Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
115      340                      345                      350
118 Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
119      355                      360                      365
122 Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
123      370                      375                      380
126 Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
127 385                      390                      395                      400
130 Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
131      405                      410                      415
134 Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
135      420                      425                      430
138 Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
139      435                      440                      445
142 Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
143      450                      455                      460
146 Phe Tyr Ile
147 465

```

150 <210> SEQ ID NO: 2

151 <211> LENGTH: 1404

152 <212> TYPE: DNA

153 <213> ORGANISM: Human

155 <400> SEQUENCE: 2

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156 atgacagagt tacctgcacc gttgtcctac ttccagaatg cacagatgtc tgaggacaac      60
158 cacctgagca atactgtacg tagccagaat gacaatagag aacggcagga gcacaacgac      120
160 agacggagcc ttggccaccc tgagccatta tctaattggac gaccccaggg taactcccgg      180
162 caggtggtgg agcaagatga ggaagaagat gaggagctga cattgaaata tggcgccaag      240
164 catgtgatca tgctctttgt ccctgtgact ctctgcatgg tgggtggtcgt ggctactatt      300
166 aagtcagtca gcttttatac ccggaaggat gggcagctaa tctatacccc attcacagaa      360
168 gataccgaga ctgtgggcca gagagccctg cactcaattc tgaatgctgc catcatgac      420
170 agtgtcattg ttgtcatgac taccctcctg gtggttctgt ataaatacag gtgtataag      480
172 gtcacccatg cctggcctat tatatcatct ctattgttgc tgttcttttt ttcattcatt      540
174 tacttggggg aagtgtttaa aacctataac gttgctgtgg actacattac tgttgcactc      600

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176 ctgatctgga attttggtgt ggtgggaatg atttccattc actggaaagg tccacttcga      660
178 ctccagcagg catatctcat tatgattagt gccctcatgg ccctgggtgt tatcaagtac      720
180 ctccctgaat ggactgcgtg gctcatcttg gctgtgattt cagtatatga tttagtggct      780
182 gttttgtgtc cgaaagggtcc acttcgtatg ctggttgaaa cagctcagga gagaaatgaa      840
184 acgctttttc cagctctcat ttactcctca acaatggtgt ggttggtgaa tatggcagaa      900
186 ggagacccgg aagctcaaag gagagtatcc aaaaattcca agtataatgc agaaagcaca      960
188 gaaagggagt cacaagacac tgttgccagag aatgatgatg gcgggttcag tgaggaatgg     1020
190 gaagcccaga gggacagtca tctagggcct catcgctcta cacctgagtc acgagctgct     1080
192 gtccaggaac tttccagcag taccctcgct ggtgaagacc cagaggaaag gggagtaaaa     1140
194 cttggattgg gagatttcat tttctacagt gttctggttg gtaaagcctc agcaacagcc     1200
196 agtggagact ggaacacaac catagcctgt ttcgtagcca tattaattgg tttgtgcctt     1260
198 acattattac tccttgccat tttcaagaaa gcattgccag ctcttccaat ctccatcacc     1320
200 tttgggcttg ttttctactt tgccacagat tatcttgtag agccttttat ggaccaatta     1380
202 gcattccatc aattttatat cttag                                     1404
205 <210> SEQ ID NO: 3
206 <211> LENGTH: 467
207 <212> TYPE: PRT
208 <213> ORGANISM: Mouse
210 <400> SEQUENCE: 3
212 Met Thr Glu Ile Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met
213 1          5          10          15
216 Ser Glu Asp Ser His Ser Ser Ser Ala Ile Arg Ser Gln Asn Asp Ser
217          20          25          30
220 Glu Glu Arg Gln Gln Gln His Asp Arg Gln Arg Leu Asp Asn Pro Glu
221          35          40          45
224 Pro Ile Ser Asn Gly Arg Pro Gln Ser Asn Ser Arg Gln Val Val Glu
225          50          55          60
228 Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
229 65          70          75          80
232 His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
233          85          90          95
236 Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
237          100         105         110
240 Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
241          115         120         125
244 Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
245          130         135         140
248 Ile Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
249 145         150         155         160
252 Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
253          165         170         175
256 Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
257          180         185         190
260 Val Asp Tyr Val Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
261          195         200         205
264 Gly Met Ile Ala Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
265          210         215         220
268 Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
269 225         230         235         240

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272 Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
 273 245 250 255
 276 Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
 277 260 265 270
 280 Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
 281 275 280 285
 284 Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
 285 290 295 300
 288 Ala Glu Arg Arg Val Pro Lys Asn Pro Lys Tyr Asn Thr Gln Arg Ala
 289 305 310 315 320
 292 Glu Arg Glu Thr Gln Asp Ser Gly Ser Gly Asn Asp Asp Gly Gly Phe
 293 325 330 335
 296 Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
 297 340 345 350
 300 Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Gly Ser Ile
 301 355 360 365
 304 Leu Thr Ser Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
 305 370 375 380
 308 Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
 309 385 390 395 400
 312 Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
 313 405 410 415
 316 Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
 317 420 425 430
 320 Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
 321 435 440 445
 324 Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
 325 450 455 460
 328 Phe Tyr Ile
 329 465

332 <210> SEQ ID NO: 4

333 <211> LENGTH: 1404

334 <212> TYPE: DNA

335 <213> ORGANISM: Mouse

337 <400> SEQUENCE: 4

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338 atgacagaga tacctgcacc tttgtcctac ttccagaatg cccagatgtc tgaggacagc      60
340 cactccagca ggcgccatccg gagccagaat gacagccaag aacggcagca gcagcatgac      120
342 aggcagagac ttgacaaccc tgagccaata tctaattgggc ggccccagag taactcaaga      180
344 caggtggtgg aacaagatga ggaggaagac gaagagctga cattgaaata tggagccaag      240
346 catgtcatca tgctctttgt ccccgtagacc ctctgcatgg tcgtcgctcgt ggccaccatc      300
348 aaatcagtca gcttctatac ccggaaggac ggtcagctaa tctacacccc attcacagaa      360
350 gacactgaga ctgtaggcca aagagccctg cactcgatcc tgaatgcggc catcatgatc      420
352 agtgtcattg tcattatgac catcctcctg gtggctcctgt ataaatacag gtgctacaag      480
354 gtcacccacg cctggcttat tatttcattc ctggtgttgc tgttcttttt ttcgttcatt      540
356 tacttagggg aagtatttaa gacctacaat gtcgccgtgg actacgttac agtagcactc      600
358 ctaatctgga attttggtgt ggtcgggatg attgccatcc actggaaagg ccccttcga      660
360 ctgcagcagg cgtatctcat tatgatcagt gccctcatgg ccttggtatt tatcaagtac      720
362 ctccccgaat ggaccgcatg gctcatcttg gctgtgattt cagtatatga tttggtggct      780
364 gttttatgtc ccaaaggccc acttcgtatg ctggttgaaa cagctcagga aagaaatgag      840

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366 actctctttc cagctcttat ctattcctca acaatgggtg ggttggtgaa tatggctgaa      900
368 ggagaccag aagcccaaag gagggtagcc aagaacccca agtataacac acaaagagcg      960
370 gagagagaga cacaggacag tgggtctggg aacgatgatg gtggcttcag tgaggagtgg     1020
372 gagggccaaa gagacagtca cctggggcct catcgctcca ctcccgagtc aagagctgct     1080
374 gtccaggaac tttctgggag cattctaacg agtgaagacc cggaggaaaag aggagtaaaa     1140
376 cttggactgg gagatttcat tttctacagt gttctggttg gtaaggcctc agcaaccgcc     1200
378 agtggagact ggaacacaa catagcctgc tttgtagcca tactgatcgg cctgtgcctt     1260
380 acattactcc tgctcgccat tttcaagaaa gcgttgccag ccctcccat ctccatcacc     1320
382 ttcgggctcg tgttctactt cgccacggat taccttgtgc agcccttcat ggaccaactt     1380
384 gcattccatc agttttatat cttag                                     1404
387 <210> SEQ ID NO: 5
388 <211> LENGTH: 25
389 <212> TYPE: DNA
390 <213> ORGANISM: Artificial
392 <220> FEATURE:
393 <223> OTHER INFORMATION: Primer
395 <400> SEQUENCE: 5
396 ggaattttgg tgtggtcggg atgat                                     25
399 <210> SEQ ID NO: 6
400 <211> LENGTH: 23
401 <212> TYPE: DNA
402 <213> ORGANISM: Artificial
404 <220> FEATURE:
405 <223> OTHER INFORMATION: Primer
407 <400> SEQUENCE: 6
408 ggtccattcg gggaggtagt tga                                     23
411 <210> SEQ ID NO: 7
412 <211> LENGTH: 36
413 <212> TYPE: DNA
414 <213> ORGANISM: Artificial
416 <220> FEATURE:
417 <223> OTHER INFORMATION: Primer
419 <400> SEQUENCE: 7
420 tgtggtcggg atgatcgcca cccactggaa aggccc                                     36
423 <210> SEQ ID NO: 8
424 <211> LENGTH: 36
425 <212> TYPE: DNA
426 <213> ORGANISM: Artificial
428 <220> FEATURE:
429 <223> OTHER INFORMATION: Primer
431 <400> SEQUENCE: 8
432 gggcctttcc agtgggtggc gatcatcccg accaca                                     36
435 <210> SEQ ID NO: 9
436 <211> LENGTH: 18
437 <212> TYPE: DNA
438 <213> ORGANISM: Artificial
440 <220> FEATURE:
441 <223> OTHER INFORMATION: Primer
443 <400> SEQUENCE: 9

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/581,528F

DATE: 09/27/2005
TIME: 15:21:57

Input Set : A:\P19743.txt
Output Set: N:\CRF4\09272005\I581528F.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:20; N Pos. 20,21,22

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22

VERIFICATION SUMMARY

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L:614 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0